

RAW SEQUENCE LISTING

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Application Serial Number: 10/516,768
Source: PCT
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PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/516,768

DATE: 06/15/2005
TIME: 14:43:37

Input Set : A:\62273715.app
Output Set: N:\CRF4\06152005\J516768.raw

3 <110> APPLICANT: MINAMINO, NAOTO
 4 KATAFUCHI, TAKESHI
 6 <120> TITLE OF INVENTION: NOVEL PEPTIDES HAVING cAMP PRODUCING ACTIVITY
 8 <130> FILE REFERENCE: 62273(71526)
 10 <140> CURRENT APPLICATION NUMBER: 10/516,768
 11 <141> CURRENT FILING DATE: 2004-12-03
 13 <150> PRIOR APPLICATION NUMBER: PCT/JP03/06641
 14 <151> PRIOR FILING DATE: 2003-05-28
 16 <150> PRIOR APPLICATION NUMBER: JP 2002-162797
 17 <151> PRIOR FILING DATE: 2002-06-04
 19 <160> NUMBER OF SEQ ID NOS: 52
 21 <170> SOFTWARE: PatentIn Ver. 3.3
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 38
 25 <212> TYPE: PRT
 26 <213> ORGANISM: Sus sp.
 28 <220> FEATURE:
 29 <223> OTHER INFORMATION: C-term may be amidated
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 35 Ser Arg Ser Gly Ser Met Val Arg Ser Asn Leu Leu Pro Thr Lys Met
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 38 Gly Phe Lys Val Phe Gly
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 42 <210> SEQ ID NO: 2
 43 <211> LENGTH: 39
 44 <212> TYPE: PRT
 45 <213> ORGANISM: Sus sp.
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 54 Gly Phe Lys Val Phe Gly Gly
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 60 <212> TYPE: DNA
 61 <213> ORGANISM: Sus sp.
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 65 gctccctcct ctgctccagt ccacctgggtt cctgctgccc gaggggcacc atgggcttct 120

(PS. 6)

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66 ggaaaatttcc gcccttcctg gttctcagca tcctggctt gtaccaggca ggcatgttcc 180
 67 acacagcacc aatgaggtct gccttggga gccctttga tcctgctacc ctctctgagg 240
 68 aggaatcacg ctccttttgc gctgcaatgg tgaatgacta tgagcagatg aaggcccgtg 300
 69 agatgcagaa gcagaggcca cagggctccg gcatcagtgt ccagaagaga tcctgcaaca 360
 70 ctgccacactg catgaccat cgctgggtgg gcttgctcag cagatctggg agcatggtga 420
 71 ggagcaacct gttgccacc aagatgggct tcaaagtctt tggtgggcgc cgcaggaact 480
 72 tttggatctg agcagtggga tgattccagg aggaaggta ctatgactct gaactctatt 540
 73 cguttaattt acaatgaaag caacctacta aaaaatagca tggaaagacat ccatgttatgc 600
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 75 aaaatcaatg catcaatgc 679
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 80 <212> TYPE: PRT
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 87 Leu Tyr Gln Ala Gly Met Phe His Thr Ala Pro Met Arg Ser Ala Phe
 88 20 25 30
 90 Gly Ser Pro Phe Asp Pro Ala Thr Leu Ser Glu Glu Glu Ser Arg Leu
 91 35 40 45
 93 Leu Leu Ala Ala Met Val Asn Asp Tyr Glu Gln Met Lys Ala Arg Glu
 94 50 55 60
 96 Met Gln Lys Gln Arg Ala Gln Gly Ser Gly Ile Ser Val Gln Lys Arg
 97 65 70 75 80
 99 Ser Cys Asn Thr Ala Thr Cys Met Thr His Arg Leu Val Gly Leu Leu
 100 85 90 95
 102 Ser Arg Ser Gly Ser Met Val Arg Ser Asn Leu Leu Pro Thr Lys Met
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 105 Gly Phe Lys Val Phe Gly Gly Arg Arg Arg Asn Phe Trp Ile
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 116 <222> LOCATION: (1730)..(1815)
 118 <220> FEATURE:
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 120 <222> LOCATION: (2323)..(2457)
 122 <220> FEATURE:
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 124 <222> LOCATION: (2754)..(2910)
 126 <400> SEQUENCE: 5
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 131 aaccgcactt ggacatggta gtcttaggg accggggatg cttgtaatg ctgactctg 180
 133 ctctacaaag atcacatagc tggggatgaa gagggatgtg agcctgcgaa accgaacagg 240

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137	gttggtgcacc accaacctcc ccacccccc ccaccccccgc catcaatgac ctcacaaatgc	360
139	ataacaagtgg ggtggcctg ttggatgctc caggttctgg acgcaagtag tgacacaatc	420
141	ctggggctca ggatcttcc tctcatttgt tgcctggagc tctgggacca cccagatcc	480
143	agagccgcgg gaataagagc agctgctggt gcgggaaagg gttagagcca ctacccacct	540
145	caagtgtctc tgccgcttct tccacagtgc catgcctga cgccaacgct gctgcctctg	600
147	ctccctcctc tgctccagtc cacctggttc ctgctgccc gtaagcccg agattcctgc	660
149	taagctgtgg ttctgtttct ctctccctc ctccttcctc ctctctctcc attggatttt	720
151	cttagctgat ctctttccc gtctcaaagt tcctgtccac ttctctctgg gtctcttcat	780
153	cctgtaatat gccttaactgc gcaattcatt cttagctctt ttcacaggta actctggatg	840
155	gtctcagttc ggggattccc tgctctactc ttccctgagct gagctgggtt ccagtcttg	900
157	ccccgcagca gacgtgttta ggtccgtt gggattttgg agctctccag gcacattcagg	960
159	gagaggagga tgcaggaata gctttgagca gaagaaactt tcatggatcc catctctct	1020
161	tacctacaag gatcgcttgc aatggggctg ggacactggga cagtgc当地 gggggcaaa	1080
163	taggtgcaat gactgagggg aaagtagcta taaaacgc当地 gccccaggta aagttctgg	1140
165	gaactcccccc tcccgacccg ccacccatt taatcttggg tcccaattta aggctgtacc	1200
167	agcttggttc ttacagggtg ctctttgcca gagtatggag cagctggaca gtaaaatttg	1260
169	gttcttcaat ttctcagggta ttccaaactgc agagatatgt cctcccaact cccctcccc	1320
171	ccagccaggt ataagcaaaa atcaggcatc aggagagatg ctgatgggtt gcactatggg	1380
173	aaaagctgtg gtgacaggtt ctgcgagttt gtcctccagg agtcccggcc aacaggttga	1440
175	aggtgagagt gtgggtgtgc tggcggggg gctatggac gagaccttcc caccaggatg	1500
177	tcctgctagg cttctttgtt aaaccaaaca tggcggc tcactggatc ttccagcagg	1560
179	ccacttggct gaggagggaa tgatggtaaa agggaaaggac acgagcagcc tgaagccagg	1620
181	aagccaggga gttggaggca gaggcaggag cagagccca gttctgtggc tcaatgaact	1680
183	tggaaactgct acaggtgggtg acattgttct tcccttgc当地 aggggcacc atg ggc ttc	1738
184	Met Gly Phe	
185	1	
187	tgg aaa ttt ccg ccc ttc ctg gtt ctc agc atc ctg gtc ctg tac cag	1786
188	Trp Lys Phe Pro Pro Phe Leu Val Leu Ser Ile Leu Val Leu Tyr Gln	
189	5 10 15	
191	gca ggc atg ttc cac aca gca cca atg ag gtaagacagc cctgccaaca	1835
192	Ala Gly Met Phe His Thr Ala Pro Met Arg	
193	20 25	
195	agcacactca cttgtatgaga atgtaatata aacgtgtata taaatttatt ataagggtggc	1895
197	tctgtatgaaac aatggatagt gccttgcgtc cctataagtt tatcataagc tttatgtgt	1955
199	cacaaagtttt gtaaatagac ataagatata cagtaactcat gattgttaat tttatataac	2015
201	ttatcaaacc tcacagcatg cttttttgtt ttcatcaaattt atttgtaccc ttagcacacg	2075
203	tatatgctca tattaccata attaagaaa tggattgtat ccaatttgcc aaatactttg	2135
205	ctagtaaattt tggttattaaa tctgtatgg gatctacaca tctcattttt caccattt	2195
207	caaactgcat taagctaaaa ttatccc attcaaacta tcagaaacca ggcaacctgg	2255
209	ctgttttatcc tgggagggg caggcaggag atcagaaccc gtttttaggc ttccctcccc	2315
211	tccttag g tct gcc ttt ggg agc cct ttt gat cct gct acc ctc tct gag	2365
212	Ser Ala Phe Gly Ser Pro Phe Asp Pro Ala Thr Leu Ser Glu	
213	30 35 40	
215	gag gaa tca cgc ctc ctt ttg gct gca atg gtg aat gac tat gag cag	2413
216	Glu Glu Ser Arg Leu Leu Ala Ala Met Val Asn Asp Tyr Glu Gln	
217	45 50 55	
219	atg aag gcc cgt gag atg cag aag cag agg gca cag ggc tcc gg	2457
220	Met Lys Ala Arg Glu Met Gln Lys Gln Arg Ala Gln Gly Ser Gly	

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221	60	65	70				
223	gtaaggttcc	ctgcccagg	acaacagggc	atccctttct	tcctctggc	agggccagga	2517
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227	ttatggcatt	tcccctgacg	gcctaggatt	ttctctgtg	atgaccttt	ctagcagaaa	2637
229	tactcaaggt	tcactggtcc	tctcaaggca	gtagtctcc	atgacgatcc	tgtcgtagag	2697
231	cacctgcact	caacctctca	ctgacgggcc	ttttcttct	ttatcccaca	aatccag c	2754
233	atc agt gtc	cag aag aga	tcc tgc aac	act gcc acc	tgc atg acc	cat	2802
234	Ile Ser Val Gln Lys Arg Ser Cys Asn Thr Ala	Thr Cys Met Thr His					
235	75	80	85	90			
237	cgg ctg gtg ggc ttg ctc	agc aga tct	ggg agc atg	gtg agg agc	acc aac		2850
238	Arg Leu Val Gly Leu Leu Ser Arg Ser Gly Ser	Met Val Arg Ser Asn					
239	95	100	105				
241	ctg ttg ccc acc aag atg ggc ttc	aaa gtc ttt	ggt ggg cgc	cgc agg			2898
242	Leu Leu Pro Thr Lys Met Gly Phe Lys Val Phe	Gly Gly Arg Arg Arg					
243	110	115	120				
245	aac ttt tgg atc tgagcagtgg	gatgattcca	ggaggaaggt	gactgccctt			2950
246	Asn Phe Trp Ile						
247	125						
249	tttgtacctt	cgggtggag	gacagaggac	tggtatgc	aggggtgc	at tccacaccct	3010
251	aaccctctgt	gagcgcatgg	gggtaaaacc	tccacatggc	aagggtccca	caccagtgtc	3070
253	tggagaaagg	actgataatc	cctataactg	aaacattggg	ctctttctct	ctgtttctcc	3130
255	agtctctccc	tgtgacactg	acatcatctg	ccagggaaata	tagaccctgt	ttacttaaaa	3190
257	cactgttccc	tggtattaa	ttggggtcca	gctctagcat	tagaatttga	aaggtatga	3250
259	ccctaccctt	ttggagcata	ccttacaatg	ttatgaactt	ggagcataga	ctcgattca	3310
261	aatactgtgt	ctgtcttcca	ctaactgtga	ccataggcaa	gtatgcctct	gaggctcagc	3370
263	ttctccctgt	aacttgaagg	caacaatagt	atcccaata	taaaaaat	ttagtataac	3430
265	atatgacaag	agcctgttaa	ctaagaat	ataacattct	gttactttt	tccctccat	3490
267	gttactatga	ctctgaactc	tacttcgtt	aatttacaat	gaaagcaacc	tactaaaaaa	3550
269	tagcatggaa	gacatccatg	tatgcatgt	tctggaaact	gaaaacactc	tttccttga	3610
271	aataaaactaa	aactaatgc	aaaataaaat	caatgcatca	atgcagttac	cttgtgtgca	3670
273	tcttttgtgt	atatgattct	ataatatgt	gcatgtctca	ttaggtttaa	ttgttagcaaa	3730
275	tctggccct	gtcagccaac	ctgttggtgg	ggcagctct	gctaaacactc	agggtcacat	3790
277	gaattc						3796
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281	<211> LENGTH: 40						
282	<212> TYPE: PRT						
283	<213> ORGANISM: Bos sp.						
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289	Ser Arg Ser Gly Ser Met Val Arg Ser Asn	Leu Leu Pro Thr Lys	Met				
290	20	25	30				
292	Gly Phe Lys Ile Phe Asn Gly Pro						
293	35	40					
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297	<211> LENGTH: 649						
298	<212> TYPE: DNA						
299	<213> ORGANISM: Bos sp.						
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302 tgtctctgcc acttctgcca gactgccact gcctgctgcc aaagctactg ctgctgtcc 60
 303 ttccctctgtc cccagccacc tggtgccggc tgtcagagag gtgtcatggg cttctggaag 120
 304 ttccccccat tcttggtcct cagcatcctg gtctgtacc aggcaggcat gttcatgca 180
 305 gcaccattca ggtctgtctt tgatggcggt tttgatcctg ctacccttggaa 240
 306 tcgcgcctcc tactggctgc gatggtaat gactacgagc agatgaggc ccgggagtgc 300
 307 gagaaggctc agaagaccga gggctcccgc atccagaaga gaggcctgcaa cactgccacc 360
 308 tgcataccatgaccc atgcctggc aggctggctg agcagatctg ggagtatgtt gaggagcaac 420
 309 ttgctgcccga ccaagatggg tttcaagatc ttcaatggc cccgcagaa ctctggttt 480
 310 taaaacagtga aatgacgctg ggaataaggt caccaggaag ctgaactcta ctttagttt 540
 311 gcatgaaggc accttacaaa aaaagaaaat agcatggaag atacccatgt atgcatacgtt 600
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 316 <211> LENGTH: 125
 317 <212> TYPE: PRT
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 324 Leu Tyr Gln Ala Gly Met Phe His Ala Ala Pro Phe Arg Ser Val Phe
 325 20 25 30
 327 Asp Gly Arg Phe Asp Pro Ala Thr Leu Asp Glu Glu Glu Ser Arg Leu
 328 35 40 45
 330 Leu Leu Ala Ala Met Val Asn Asp Tyr Glu Gln Met Arg Ala Arg Glu
 331 50 55 60
 333 Ser Glu Lys Ala Gln Lys Thr Glu Gly Ser Arg Ile Gln Lys Arg Ala
 334 65 70 75 80
 336 Cys Asn Thr Ala Thr Cys Met Thr His Arg Leu Ala Gly Trp Leu Ser
 337 85 90 95
 339 Arg Ser Gly Ser Met Val Arg Ser Asn Leu Leu Pro Thr Lys Met Gly
 340 100 105 110
 342 Phe Lys Ile Phe Asn Gly Pro Arg Arg Asn Ser Trp Phe
 343 115 120 125
 346 <210> SEQ ID NO: 9
 347 <211> LENGTH: 38
 348 <212> TYPE: PRT
 349 <213> ORGANISM: Canis sp.
 351 <400> SEQUENCE: 9
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 355 Ser Arg Ala Gly Ser Val Ala Asn Thr Asn Leu Leu Pro Thr Ser Met
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 358 Gly Phe Lys Val Tyr Asn
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 362 <210> SEQ ID NO: 10
 363 <211> LENGTH: 686
 364 <212> TYPE: DNA
 365 <213> ORGANISM: Canis sp.
 367 <400> SEQUENCE: 10
 368 tctgccacat ccacggtgcc atgcctgac atcgacgccc aacactgcca cagctggcgc 60

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:31; N Pos. 9,12,15

Seq#:32; N Pos. 6,15

Seq#:33; Xaa Pos. 2,7

Seq#:34; Xaa Pos. 2,7

VERIFICATION SUMMARY
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L:1361 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:0
L:1384 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:0
L:1403 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:0
L:1426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:0